



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/502,244

DATE: 07/29/2004
TIME: 16:11:53

Input Set : A:\seq_1st_US.txt
Output Set: N:\CRF4\07292004\J502244.raw

5 <110> APPLICANT: Carmeliet, Peter
6 Moons, Lieve
9 <120> TITLE OF INVENTION: A NOVEL TARGET TO INHIBIT ANGIOGENESIS
13 <130> FILE REFERENCE: DECLE70.003APC
C--> 16 <140> CURRENT APPLICATION NUMBER: US/10/502,244
C--> 16 <141> CURRENT FILING DATE: 2004-07-22
16 <150> PRIOR APPLICATION NUMBER: EP02075544.3
18 <151> PRIOR FILING DATE: 2002-02-08
22 <150> PRIOR APPLICATION NUMBER: EP02077742.1
24 <151> PRIOR FILING DATE: 2002-07-09
28 <150> PRIOR APPLICATION NUMBER: EP03100148.0
30 <151> PRIOR FILING DATE: 2003-01-24
34 <160> NUMBER OF SEQ ID NOS: 2
38 <170> SOFTWARE: PatentIn version 3.1
42 <210> SEQ ID NO: 1
44 <211> LENGTH: 3794
46 <212> TYPE: DNA
48 <213> ORGANISM: Homo sapiens
52 <220> FEATURE:
54 <221> NAME/KEY: CDS
56 <222> LOCATION: (38)..(2635)
58 <223> OTHER INFORMATION:
W--> 62 <400> 1

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67 tcc ctg ttg ctg ctg ggg ctg tgc ggg aac tcc ttt tca gga ggg cag	103
68 Ser Leu Leu Leu Gly Leu Cys Gly Asn Ser Phe Ser Gly Gly Gln	
69 10 15 20	
71 cct tca tcc aca gat gct cct aag gct tgg aat tat gaa ttg cct gca	151
72 Pro Ser Ser Thr Asp Ala Pro Lys Ala Trp Asn Tyr Glu Leu Pro Ala	
73 25 30 35	
75 aca aat tat gag acc caa gac tcc cat aaa gct gga ccc att ggc att	199
76 Thr Asn Tyr Glu Thr Gln Asp Ser His Lys Ala Gly Pro Ile Gly Ile	
77 40 45 50	
79 ctc ttt gaa cta gtg cat atc ttt ctc tat gtg gta cag ccg cgt gat	247
80 Leu Phe Glu Leu Val His Ile Phe Leu Tyr Val Val Gln Pro Arg Asp	
81 55 60 65 70	
83 ttc cca gaa gat act ttg aga aaa ttc tta cag aag gca tat gaa tcc	295
84 Phe Pro Glu Asp Thr Leu Arg Lys Phe Leu Gln Lys Ala Tyr Glu Ser	
85 75 80 85	
87 aaa att gat tat gac aag cca gaa act gta atc tta ggt cta aag att	343
88 Lys Ile Asp Tyr Asp Lys Pro Glu Thr Val Ile Leu Gly Leu Lys Ile	

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91	gtc tac tat gaa gca ggg att att cta tgc tgt gtc ctg ggg ctg ctg			391
92	Val Tyr Tyr Glu Ala Gly Ile Ile Leu Cys Cys Val Leu Gly Leu Leu			
93	105	110	115	
95	ttt att att ctg atg cct ctg gtg ggg tat ttc ttt tgt atg tgt cgt			439
96	Phe Ile Ile Leu Met Pro Leu Val Gly Tyr Phe Phe Cys Met Cys Arg			
97	120	125	130	
99	tgc tgt aac aaa tgt ggt gga gaa atg cac cag cga cag aag gaa aat			487
100	Cys Cys Asn Lys Cys Gly Gly Glu Met His Gln Arg Gln Lys Glu Asn			
101	135	140	145	150
103	ggg ccc ttc ctg agg aaa tgc ttt gca atc tcc ctg ttg gtg att tgt			535
104	Gly Pro Phe Leu Arg Lys Cys Phe Ala Ile Ser Leu Leu Val Ile Cys			
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108	Ile Ile Ile Ser Ile Gly Ile Phe Tyr Gly Phe Val Ala Asn His Gln			
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111	gta aga acc cgg atc aaa agg agt cgg aaa ctg gca gat agc aat ttc			631
112	Val Arg Thr Arg Ile Lys Arg Ser Arg Lys Leu Ala Asp Ser Asn Phe			
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115	aag gac ttg cga act ctc ttg aat gaa act cca gag caa atc aaa tat			679
116	Lys Asp Leu Arg Thr Leu Leu Asn Glu Thr Pro Glu Gln Ile Lys Tyr			
117	200	205	210	
119	ata ttg gcc cag tac aac act acc aag gac aag gcg ttc aca gat ctg			727
120	Ile Leu Ala Gln Tyr Asn Thr Thr Lys Asp Lys Ala Phe Thr Asp Leu			
121	215	220	225	230
123	aac agt atc aat tca gtg cta gga ggc gga att ctt gac cga ctg aga			775
124	Asn Ser Ile Asn Ser Val Leu Gly Gly Ile Leu Asp Arg Leu Arg			
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131	atc aag gag acc aaa gag gcg ttg gag aac atg aac agc acc ttg aag			871
132	Ile Lys Glu Thr Lys Glu Ala Leu Glu Asn Met Asn Ser Thr Leu Lys			
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135	agc ttg cac caa caa agt aca cag ctt agc agc agt ctg acc agc gtg			919
136	Ser Leu His Gln Gln Ser Thr Gln Leu Ser Ser Leu Thr Ser Val			
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139	aaa act agc ctg cgg tca tct ctc aat gac cct ctg tgc ttg gtg cat			967
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143	cca tca agt gaa acc tgc aac agc atc aga ttg tct cta agc cag ctg			1015
144	Pro Ser Ser Glu Thr Cys Asn Ser Ile Arg Leu Ser Leu Ser Gln Leu			
145	315	320	325	
147	aat agc aac cct gaa ctg agg cag ctt cca ccc gtg gat gca gaa ctt			1063
148	Asn Ser Asn Pro Glu Leu Arg Gln Leu Pro Pro Val Asp Ala Glu Leu			
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151	gac aac gtt aat aac gtt ctt agg aca gat ttg gat ggc ctg gtc caa			1111
152	Asp Asn Val Asn Asn Val Leu Arg Thr Asp Leu Asp Gly Leu Val Gln			
153	345	350	355	

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155 cag ggc tat caa tcc ctt aat gat ata cct gac aga gta caa cgc caa	1159
156 Gln Gly Tyr Gln Ser Leu Asn Asp Ile Pro Asp Arg Val Gln Arg Gln	
157 360 365 370	
159 acc acg act gtc gta gca ggt atc aaa agg gtc ttg aat tcc att ggt	1207
160 Thr Thr Val Val Ala Gly Ile Lys Arg Val Leu Asn Ser Ile Gly	
161 375 380 385 390	
163 tca gat atc gac aat gta act cag cgt ctt cct att cag gat ata ctc	1255
164 Ser Asp Ile Asp Asn Val Thr Gln Arg Leu Pro Ile Gln Asp Ile Leu	
165 395 400 405	
167 tca gca ttc tct gtt tat gtt aat aac act gaa agt tac atc cac aga	1303
168 Ser Ala Phe Ser Val Tyr Val Asn Asn Thr Glu Ser Tyr Ile His Arg	
169 410 415 420	
171 aat tta cct aca ttg gaa gag tat gat tca tac tgg tgg ctg ggt ggc	1351
172 Asn Leu Pro Thr Leu Glu Glu Tyr Asp Ser Tyr Trp Trp Leu Gly Gly	
173 425 430 435	
175 ctg gtc atc tgc tct ctg ctg acc ctc atc gtg att ttt tac tac ctg	1399
176 Leu Val Ile Cys Ser Leu Leu Thr Leu Ile Val Ile Phe Tyr Tyr Leu	
177 440 445 450	
179 ggc tta ctg tgt ggc gtg tgc ggc tat gac agg cat gcc acc ccg acc	1447
180 Gly Leu Leu Cys Gly Val Cys Gly Tyr Asp Arg His Ala Thr Pro Thr	
181 455 460 465 470	
183 acc cga ggc tgt gtc tcc aac acc gga ggc gtc ttc ctc atg gtt gga	1495
184 Thr Arg Gly Cys Val Ser Asn Thr Gly Gly Val Phe Leu Met Val Gly	
185 475 480 485	
187 gtt gga tta agt ttc ctc ttt tgc tgg ata ttg atg atc att gtg gtt	1543
188 Val Gly Leu Ser Phe Leu Phe Cys Trp Ile Leu Met Ile Ile Val Val	
189 490 495 500	
191 ctt acc ttt gtc ttt ggt gca aat gtg gaa aaa ctg atc tgt gaa cct	1591
192 Leu Thr Phe Val Gly Ala Asn Val Glu Lys Leu Ile Cys Glu Pro	
193 505 510 515	
195 tac acg agc aag gaa tta ttc cgg gtt ttg gat aca ccc tac tta cta	1639
196 Tyr Thr Ser Lys Glu Leu Phe Arg Val Leu Asp Thr Pro Tyr Leu Leu	
197 520 525 530	
199 aat gaa gac tgg gaa tac tat ctc tct ggg aag cta ttt aat aaa tca	1687
200 Asn Glu Asp Trp Glu Tyr Tyr Leu Ser Gly Lys Leu Phe Asn Lys Ser	
201 535 540 545 550	
203 aaa atg aag ctc act ttt gaa caa gtt tac agt gac tgc aaa aaa aat	1735
204 Lys Met Lys Leu Thr Phe Glu Gln Val Tyr Ser Asp Cys Lys Lys Asn	
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207 aga ggc act tac ggc act ctt cac ctg cag aac agc ttc aat atc agt	1783
208 Arg Gly Thr Tyr Gly Thr Leu His Leu Gln Asn Ser Phe Asn Ile Ser	
209 570 575 580	
211 gaa cat ctc aac att aat gag cat act gga agc ata agc agt gaa ttg	1831
212 Glu His Leu Asn Ile Asn Glu His Thr Gly Ser Ile Ser Ser Glu Leu	
213 585 590 595	
215 gaa agt ctg aag gta aat ctt aat atc ttt ctg ttg ggt gca gca gga	1879
216 Glu Ser Leu Lys Val Asn Leu Asn Ile Phe Leu Leu Gly Ala Ala Gly	
217 600 605 610	
219 aga aaa aac ctt cag gat ttt gct tgt gga ata gac aga atg aat	1927

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220 Arg Lys Asn Leu Gln Asp Phe Ala Ala Cys Gly Ile Asp Arg Met Asn	
221 615 620 625 630	
223 tat gac agc tac ttg gct cag act ggt aaa tcc ccc gca gga gtg aat	1975
224 Tyr Asp Ser Tyr Leu Ala Gln Thr Gly Lys Ser Pro Ala Gly Val Asn	
225 635 640 645	
227 ctt tta tca ttt gca tat gat cta gaa gca aaa gca aac agt ttg ccc	2023
228 Leu Leu Ser Phe Ala Tyr Asp Leu Glu Ala Lys Ala Asn Ser Leu Pro	
229 650 655 660	
231 cca gga aat ttg agg aac tcc ctg aaa aga gat gca caa act att aaa	2071
232 Pro Gly Asn Leu Arg Asn Ser Leu Lys Arg Asp Ala Gln Thr Ile Lys	
233 665 670 675	
235 aca att cac cag caa cga gtc ctt cct ata gaa caa tca ctg agc act	2119
236 Thr Ile His Gln Gln Arg Val Leu Pro Ile Glu Gln Ser Leu Ser Thr	
237 680 685 690	
239 cta tac caa agc gtc aag ata ctt caa cgc aca ggg aat gga ttg ttg	2167
240 Leu Tyr Gln Ser Val Lys Ile Leu Gln Arg Thr Gly Asn Gly Leu Leu	
241 695 700 705 710	
243 gag aga gta act agg att cta gct tct ctg gat ttt gct cag aac ttc	2215
244 Glu Arg Val Thr Arg Ile Leu Ala Ser Leu Asp Phe Ala Gln Asn Phe	
245 715 720 725	
247 atc aca aac aat act tcc tct gtt att att gag gaa act aag aag tat	2263
248 Ile Thr Asn Asn Thr Ser Ser Val Ile Ile Glu Glu Thr Lys Lys Tyr	
249 730 735 740	
251 ggg aga aca ata ata gga tat ttt gaa cat tat ctg cag tgg atc gag	2311
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253 745 750 755	
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256 Phe Ser Ile Ser Glu Lys Val Ala Ser Cys Lys Pro Val Ala Thr Ala	
257 760 765 770	
259 cta gat act gct gtt gat gtc ttt ctg tgt agc tac att atc gac ccc	2407
260 Leu Asp Thr Ala Val Asp Val Phe Leu Cys Ser Tyr Ile Ile Asp Pro	
261 775 780 785 790	
263 ttg aat ttg ttt tgg ttt ggc ata gga aaa gct act gta ttt tta ctt	2455
264 Leu Asn Leu Phe Trp Phe Gly Ile Gly Lys Ala Thr Val Phe Leu Leu	
265 795 800 805	
267 ccg gct cta att ttt gcg gta aaa ctg gct aag tac tat cgt cga atg	2503
268 Pro Ala Leu Ile Phe Ala Val Lys Leu Ala Lys Tyr Tyr Arg Arg Met	
269 810 815 820	
271 gat tcg gag gac gtg tac gat gat gtt gaa act ata ccc atg aaa aat	2551
272 Asp Ser Glu Asp Val Tyr Asp Asp Val Glu Thr Ile Pro Met Lys Asn	
273 825 830 835	
275 atg gaa aat ggt aat aat ggt tat cat aaa gat cat gta tat ggt att	2599
276 Met Glu Asn Gly Asn Asn Gly Tyr His Lys Asp His Val Tyr Gly Ile	
277 840 845 850	
279 cac aat cct gtt atg aca agc cca tca caa cat tga tagctgatgt	2645
280 His Asn Pro Val Met Thr Ser Pro Ser Gln His	
281 855 860 865	
283 tgaaaactgct tgagcatcag gataactcaa gtggaaagga tcacagattt ttggtagttt	2705
285 ctgggtctac aaggacttccaaatccagg agcaacgcca gtggcaacgt agtgactcag	2765

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299	ggactttctt	ctaaatgagc	taaataaagt	accattgact	tcttggtgct	gttggaaaata	3185									
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377						165			170				175			
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L:16 M:270 C: Current Application Number differs, Replaced Current Application No

L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:62 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:58